<110> Chiang, Lillian Wei-Ming

<120> NARC8 Programmed Cell
 Death-Associated Molecule and Uses Thereof

<130> 35800/207197

<150> 09/692,785
<151> 2000-10-20

<150> 60/161,188
<151> 1999-10-22

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1507
<212> DNA
<213> Homo sapeins

<220>
<221> CDS
<222> (368)...(1261)

<400> 1
gttggagcga gcatgtgggt ctgcagtacc ctgtggcggg tgcgaacccc cgcccggcag   60
tggcggggggc tgctcccagc ttctggctgt cacggacctg ccgcctcctc ctactccgca   120
tccgccgagc ctgcccgggt ccgggcgctt gtctatgggc accacgggga tccagccaag   180
gtcgtcgaaa ccgtaattcc tgggcacaca tggcagctca gaaatgttgc ctgacctact   240
ttgaggagat gatttgagcg aaacacccat tctagcctgg atgacatgaa catctccgtt   300
tggctttgtg cttagactca agaacctgga gctagctgct gtgagaggat cagatgtccg   360
tgtgaag atg ctg gcg gcc cct atc aat cca tct gac ata aat atg atc   409
        Met Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile
         1   5   10

caa gga aac tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac   457
Gln Gly Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn
 15   20   25   30

gaa ggt gtt gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg   505
Glu Gly Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu
                35   40   45

aag cca gga gac tgg gtg att cca gca aat gct ggt tta gga acc tgg   553
Lys Pro Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp
            50   55   60

cgg acc gag gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt   601
Arg Thr Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser
            65   70   75

```
gac atc cct ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca       649
Asp Ile Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr
    80                  85                  90

gcc tac agg atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct       697
Ala Tyr Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser
95                  100                 105                 110

gtc atc cag aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag       745
Val Ile Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln
                115                 120                 125

atc gcc gca gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga       793
Ile Ala Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg
            130                 135                 140

cct gat atc cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag       841
Pro Asp Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu
            145                 150                 155

cat gtc atc aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc       889
His Val Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe
    160                 165                 170

ttt aag gac atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg       937
Phe Lys Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly
175                 180                 185                 190

aaa agc tcc aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg       985
Lys Ser Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met
                195                 200                 205

gta acc tat ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc      1033
Val Thr Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser
                210                 215                 220

ctg ctc att ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag      1081
Leu Leu Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln
            225                 230                 235

tgg aag aag gat cac agt cca gac cag ttc aag gag ctg atc ctc aca      1129
Trp Lys Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr
    240                 245                 250

ctg tgc gat ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc      1177
Leu Cys Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser
255                 260                 265                 270

cag gtc ccg ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag      1225
Gln Val Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys
                275                 280                 285

ccc ttc ata tct tca aag cag att ctc acc atg tga tcatcccaaa          1271
Pro Phe Ile Ser Ser Lys Gln Ile Leu Thr Met  *
                290                 295
```

2

```
agagctggag tgacatggga ggggaggcgg atctgagggg ctgggtgcag gcccctcagt    1331
tggggctccc accttcccca gactactgtt ctcctcactg cctcttccta ttaggaggat    1391
ggtgaagcca gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac    1451
tctcccttcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa        1507
```

```
<210> 2
<211> 297
<212> PRT
<213> Homo sapiens

<400> 2
Met Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly
 1               5                  10                  15
Asn Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly
              20                  25                  30
Val Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro
          35                  40                  45
Gly Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr
      50                  55                  60
Glu Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile
65                  70                  75                  80
Pro Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr
                  85                  90                  95
Arg Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile
              100                 105                 110
Gln Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala
          115                 120                 125
Ala Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp
      130                 135                 140
Ile Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val
145                 150                 155                 160
Ile Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys
              165                 170                 175
Asp Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser
              180                 185                 190
Ser Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr
          195                 200                 205
Tyr Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu
      210                 215                 220
Ile Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys
225                 230                 235                 240
Lys Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys
              245                 250                 255
Asp Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val
              260                 265                 270
Pro Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe
          275                 280                 285
Ile Ser Ser Lys Gln Ile Leu Thr Met
      290                 295
```

```
<210> 3
<211> 894
<212> DNA
<213> Homo sapiens

<400> 3
atgctggcgg cccctatcaa tccatctgac ataaatatga tccaggaaa ctacggactc    60
```

3

```
cttcctgaac tgcctgctgt tggagggaac gaaggtgttg cacaggtggt agcggtgggc    120
agcaatgtga ccgggctgaa gccaggagac tgggtgattc agcaaatgc tggtttagga     180
acctggcgga ccgaggctgt gttcagcgag gaagcactga tccaagttcc gagtgacatc     240
cctcttcaga gcgctgccac cctgggtgtc aatccctgca cagcctacag gatgttgatg     300
gatttcgagc aactgcagcc aggggattct gtcatccaga atgcatccaa cagcggagtg     360
gggcaagcgg tcatccagat cgccgcagcc ctgggcctaa gaaccatcaa tgtggtccga     420
gacagacctg atatccagaa gctgagtgac agactgaaga gtctggggggc tgagcatgtc    480
atcacagaag aggagctaag aaggcccgaa atgaaaaact tctttaagga catgccccag     540
ccacggcttg ctctcaactg tgttggtggg aaaagctcca cagagctgct gcggcagtta     600
gcgcgtggag gaaccatggt aacctatggg gggatggcca agcagcccgt cgtagcctct     660
gtgagcctgc tcatttttaa ggatctcaaa cttcgaggct tttggttgtc ccagtggaag     720
aaggatcaca gtccagacca gttcaaggag ctgatcctca cactgtgcga tctcatccgc     780
cgaggccagc tcacagcccc tgcctgctcc caggtcccgc tgcaggacta ccagtctgcc     840
ttggaagcct ccatgaagcc cttcatatct tcaaagcaga ttctcaccat gtga           894
```

<210> 4
<211> 1380
<212> DNA
<213> Homo sapeins

<220>
<221> CDS
<222> (13)...(1134)

<400> 4
```
attggagcga gc atg tgg gtc tgc agt acc ctg tgg cgg gtg cga acc ccc     51
           Met Trp Val Cys Ser Thr Leu Trp Arg Val Arg Thr Pro
            1               5                  10


gcc cgg cag tgg cgg ggg ctg ctc cca gct tct ggc tgt cac gga cct     99
Ala Arg Gln Trp Arg Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro
    15                  20                  25


gcc gcc tcc tcc tac tcc gca tcc gcc gag cct gcc cgg gtc cgg gcg    147
Ala Ala Ser Ser Tyr Ser Ala Ser Ala Glu Pro Ala Arg Val Arg Ala
30                  35                  40                  45


ctt gtc tat ggg cac cac ggg gat cca gcc aag gtc gtc gaa ctc aag    195
Leu Val Tyr Gly His His Gly Asp Pro Ala Lys Val Val Glu Leu Lys
                50                  55                  60


aac ctg gag cta gct gct gtg aga gga tca gat gtc cgt gtg aag atg    243
Asn Leu Glu Leu Ala Ala Val Arg Gly Ser Asp Val Arg Val Lys Met
            65                  70                  75


ctg gcg gcc cct atc aat cca tct gac ata aat atg atc caa gga aac    291
Leu Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly Asn
            80                  85                  90


tac gga ctc ctt cct gaa ctg cct gct gtt gga ggg aac gaa ggt gtt    339
Tyr Gly Leu Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly Val
        95                  100                 105


gca cag gtg gta gcg gtg ggc agc aat gtg acc ggg ctg aag cca gga    387
Ala Gln Val Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro Gly
110                 115                 120                 125
```

4

```
gac tgg gtg att cca gca aat gct ggt tta gga acc tgg cgg acc gag       435
Asp Trp Val Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr Glu
            130                 135                 140

gct gtg ttc agc gag gaa gca ctg atc caa gtt ccg agt gac atc cct       483
Ala Val Phe Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro
            145                 150                 155

ctt cag agc gct gcc acc ctg ggt gtc aat ccc tgc aca gcc tac agg       531
Leu Gln Ser Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg
            160                 165                 170

atg ttg atg gat ttc gag caa ctg cag cca ggg gat tct gtc atc cag       579
Met Leu Met Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln
            175                 180                 185

aat gca tcc aac agc gga gtg ggg caa gcg gtc atc cag atc gcc gca       627
Asn Ala Ser Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala
190                 195                 200                 205

gcc ctg ggc cta aga acc atc aat gtg gtc cga gac aga cct gat atc       675
Ala Leu Gly Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile
                210                 215                 220

cag aag ctg agt gac aga ctg aag agt ctg ggg gct gag cat gtc atc       723
Gln Lys Leu Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile
                225                 230                 235

aca gaa gag gag cta aga agg ccc gaa atg aaa aac ttc ttt aag gac       771
Thr Glu Glu Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp
                240                 245                 250

atg ccc cag cca cgg ctt gct ctc aac tgt gtt ggt ggg aaa agc tcc       819
Met Pro Gln Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser
            255                 260                 265

aca gag ctg ctg cgg cag tta gcg cgt gga gga acc atg gta acc tat       867
Thr Glu Leu Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr
270                 275                 280                 285

ggg ggg atg gcc aag cag ccc gtc gta gcc tct gtg agc ctg ctc att       915
Gly Gly Met Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile
                290                 295                 300

ttt aag gat ctc aaa ctt cga ggc ttt tgg ttg tcc cag tgg aag aag       963
Phe Lys Asp Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys
                305                 310                 315

gat cac agt cca gac cag ttc aag gag ctg atc ctc aca ctg tgc gat      1011
Asp His Ser Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp
            320                 325                 330

ctc atc cgc cga ggc cag ctc aca gcc cct gcc tgc tcc cag gtc ccg      1059
Leu Ile Arg Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro
335                 340                 345

ctg cag gac tac cag tct gcc ttg gaa gcc tcc atg aag ccc ttc ata      1107
```

5

```
Leu Gln Asp Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile
350                 355                 360                 365


tct tca aag cag att ctc acc atg tga tcatcccaaa agagctggag          1154
Ser Ser Lys Gln Ile Leu Thr Met  *
                370


tgacatggga ggggaggcgg atctgagggg ctgggtgcag gcccctcagt tggggctccc   1214
accttcccca gactactgtt ctcctcactg cctcttccta ttaggaggat ggtgaagcca   1274
gccacggttt tccccagggc cagccttaag gtatctaata aagtctgaac tctcccttcc   1334
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa                  1380


<210> 5
<211> 373
<212> PRT
<213> Homo sapiens


<400> 5
Met Trp Val Cys Ser Thr Leu Trp Arg Val Arg Thr Pro Ala Arg Gln
 1               5                  10                  15
Trp Arg Gly Leu Leu Pro Ala Ser Gly Cys His Gly Pro Ala Ala Ser
            20                  25                  30
Ser Tyr Ser Ala Ser Ala Glu Pro Ala Arg Val Arg Ala Leu Val Tyr
        35                  40                  45
Gly His His Gly Asp Pro Ala Lys Val Val Glu Leu Lys Asn Leu Glu
    50                  55                  60
Leu Ala Ala Val Arg Gly Ser Asp Val Arg Val Lys Met Leu Ala Ala
65                  70                  75                  80
Pro Ile Asn Pro Ser Asp Ile Asn Met Ile Gln Gly Asn Tyr Gly Leu
                85                  90                  95
Leu Pro Glu Leu Pro Ala Val Gly Gly Asn Glu Gly Val Ala Gln Val
            100                 105                 110
Val Ala Val Gly Ser Asn Val Thr Gly Leu Lys Pro Gly Asp Trp Val
        115                 120                 125
Ile Pro Ala Asn Ala Gly Leu Gly Thr Trp Arg Thr Glu Ala Val Phe
    130                 135                 140
Ser Glu Glu Ala Leu Ile Gln Val Pro Ser Asp Ile Pro Leu Gln Ser
145                 150                 155                 160
Ala Ala Thr Leu Gly Val Asn Pro Cys Thr Ala Tyr Arg Met Leu Met
                165                 170                 175
Asp Phe Glu Gln Leu Gln Pro Gly Asp Ser Val Ile Gln Asn Ala Ser
            180                 185                 190
Asn Ser Gly Val Gly Gln Ala Val Ile Gln Ile Ala Ala Ala Leu Gly
        195                 200                 205
Leu Arg Thr Ile Asn Val Val Arg Asp Arg Pro Asp Ile Gln Lys Leu
    210                 215                 220
Ser Asp Arg Leu Lys Ser Leu Gly Ala Glu His Val Ile Thr Glu Glu
225                 230                 235                 240
Glu Leu Arg Arg Pro Glu Met Lys Asn Phe Phe Lys Asp Met Pro Gln
                245                 250                 255
Pro Arg Leu Ala Leu Asn Cys Val Gly Gly Lys Ser Ser Thr Glu Leu
            260                 265                 270
Leu Arg Gln Leu Ala Arg Gly Gly Thr Met Val Thr Tyr Gly Gly Met
        275                 280                 285
Ala Lys Gln Pro Val Val Ala Ser Val Ser Leu Leu Ile Phe Lys Asp
    290                 295                 300
Leu Lys Leu Arg Gly Phe Trp Leu Ser Gln Trp Lys Lys Asp His Ser
```

6

```
305                      310                      315                      320
Pro Asp Gln Phe Lys Glu Leu Ile Leu Thr Leu Cys Asp Leu Ile Arg
                    325             330             335
Arg Gly Gln Leu Thr Ala Pro Ala Cys Ser Gln Val Pro Leu Gln Asp
                340             345             350
Tyr Gln Ser Ala Leu Glu Ala Ser Met Lys Pro Phe Ile Ser Ser Lys
        355             360             365
Gln Ile Leu Thr Met
    370


<210> 6
<211> 1122
<212> DNA
<213> Homo sapeins

<400> 6
atgtgggtct gcagtaccct gtggcgggtg cgaacccccg cccggcagtg gcgggggctg       60
ctcccagctt ctggctgtca cggacctgcc gcctcctcct actccgcatc cgccgagcct      120
gcccgggtcc gggcgcttgt ctatgggcac cacggggatc cagccaaggt cgtcgaactc      180
aagaacctgg agctagctgc tgtgagagga tcagatgtcc gtgtgaagat gctggcggcc      240
cctatcaatc catctgacat aaatatgatc caaggaaact acggactcct tcctgaactg      300
cctgctgttg gagggaacga aggtgttgca caggtggtag cggtgggcag caatgtgacc      360
gggctgaagc caggagactg ggtgattcca gcaaatgctg gtttaggaac ctggcggacc      420
gaggctgtgt tcagcgagga agcactgatc caagttccga gtgacatccc tcttcagagc      480
gctgccaccc tgggtgtcaa tccctgcaca gcctacagga tgttgatgga tttcgagcaa      540
ctgcagccag gggattctgt catccagaat gcatccaaca gcggagtggg gcaagcggtc      600
atccagatcg ccgcagccct gggcctaaga accatcaatg tggtccgaga cagacctgat      660
atccagaagc tgagtgacag actgaagagt ctggggggctg agcatgtcat cacagaagag      720
gagctaagaa ggcccgaaat gaaaaacttc tttaaggaca tgccccagcc acggcttgct      780
ctcaactgtg ttggtgggaa aagctccaca gagctgctgc ggcagttagc gcgtggagga      840
accatggtaa cctatggggg gatggccaag cagcccgtcg tagcctctgt gagcctgctc      900
atttttaagg atctcaaact tcgaggcttt tggttgtccc agtggaagaa ggatcacagt      960
ccagaccagt tcaaggagct gatcctcaca ctgtgcgatc tcatccgccg aggccagctc     1020
acagcccctg cctgctccca ggtcccgctg caggactacc agtctgcctt ggaagcctcc     1080
atgaagccct tcatatcttc aaagcagatt ctcaccatgt ga                        1122


<210> 7
<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Zinc-binding dehydrogenase consensus sequence

<400> 7
Pro Leu Glu Val Glu Glu Val Pro Val Pro Glu Pro Gly Pro Gly Glu
  1               5              10              15
Val Leu Val Lys Val Lys Ala Ala Gly Ile Cys Gly Ser Asp Leu His
            20              25              30
Ile Tyr Lys Gly Gly Leu Gly Leu Met Tyr Pro Gly Pro Gly Asp Gly
        35              40              45
Thr His Leu Phe Pro Val Lys Leu Pro Leu Val Leu Gly His Glu Gly
    50              55              60
Ala Gly Val Val Glu Glu Val Gly Ser Gly Val Thr Gly Phe Lys Leu
65              70              75              80
Lys Val Gly Lys Phe Lys Val Gly Asp Arg Val Val Val Leu Pro Leu
            85              90              95
```

7

```
Val Gly Cys Cys Gly Arg Gly Ser Ala Glu Cys Glu Phe Cys Lys Gly
         100                     105                 110
Ser Gly Arg Glu Asn Leu Cys Pro Lys Gly Arg Ala Thr Gly Pro Gly
         115                 120                 125
Lys Gly Leu Met Pro Asn Asp Gly Phe Gly Gly Phe Thr Pro Lys Lys
         130             135                 140
Gln Gly Ala Pro Cys Lys Gly Lys Asp Gly Tyr His Phe Met Gly Asp
145                 150                 155                 160
Gly Gly Phe Ala Glu Tyr Val Val Val Pro Ala Arg Arg Asn Asp Tyr
             165                 170                 175
Phe Val Val Lys Ile Pro Asp Gly Leu Asp Asp Glu Ile Pro Leu Glu
             180                 185                 190
Glu Ala Glu Ala Ala Ala Leu Leu Gly Cys Ala Gly Leu Thr Ala Tyr
             195                 200                 205
Gly Ala Leu Val Arg Ala Ala Lys Val Gly Ser Leu Pro Pro Gly Asp
         210                 215                 220
Thr Val Leu Val His Gly Ala Gly Gly Gly Val Gly Leu Ala Ala Val
225                 230                 235                 240
Gln Leu Ala Lys Ala Ala Gly Ala Ala Arg Val Ile Ala Val Asp Ser
             245                 250                 255
Ser Glu Asp Lys Lys Leu Glu Leu Ala Lys Glu Leu Gly Ala Asp Leu
             260                 265                 270
Asp Ala Asp Phe Val Asn Asn Ser Lys Gly Leu Pro Thr Val Asn Asp
         275                 280                 285
Asp Arg Lys Glu Asp Phe Val Glu Ala Ile Lys Glu Leu Thr Gly Gly
         290                 295                 300
Arg Asn Gly Ala Gly Gly Val Asp Val Val Leu Asp Cys Val Gly Ile
305                 310                 315                 320
Gly Leu Gly Gly Ala Thr Leu Asp Ala Ala Leu Ala Leu Leu Lys Pro
             325                 330                 335
Gly Gly Arg Leu Val Val Val Gly Pro Lys Val Ala Val Gly Val Pro
             340                 345                 350
Gly Gly Gly Ala Pro Ile Pro Leu Leu Leu Leu Lys Glu Glu Glu Lys
             355                 360                 365
Leu Tyr Glu Arg Ser Ile Lys Gly Ser Phe Leu Gly Gly Arg Lys Pro
         370                 375                 380
Arg Leu Ser Val Leu Ser Val Asp Thr Thr Pro Asp Glu Leu Arg Glu
385                 390                 395                 400
Ala Leu Asp Leu Leu Ala Ser Gly Ile Lys Asp Lys Asn Gly Lys Gly
             405                 410                 415
Val Leu Asp Pro Leu Ile Thr His Thr Leu Pro Pro Leu Asp Asp Ser
             420                 425                 430
Leu Glu Glu Ala Asn Glu Ala Phe Glu Leu Leu Glu Ser Gly Lys His
         435                 440                 445
Gly Lys Val Val Leu Ile Pro
         450                 455
```

8